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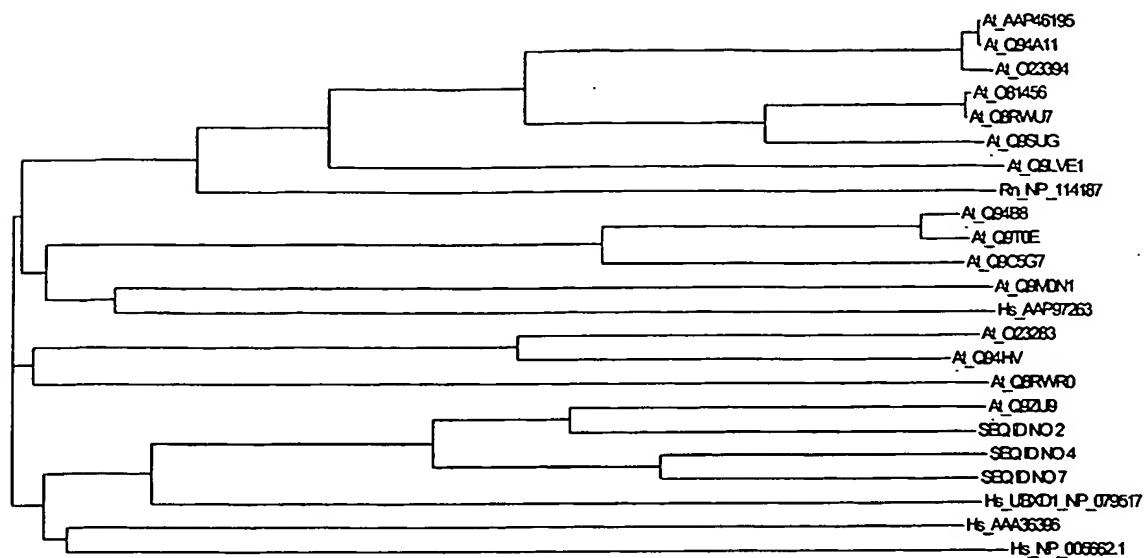


FIGURE 1 A

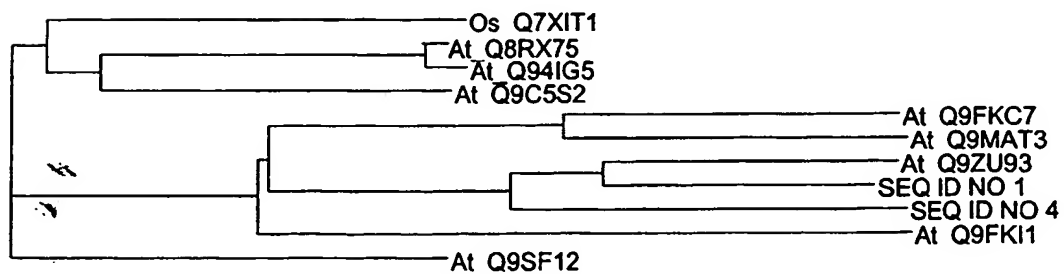


FIGURE 1B

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Consensus terms for the UBX domain

YJE8_YEAST	KGFLAQ-NYCTLQLKLPNGYTISNTFP-PQTKLHKVRMWL-----DYNCYDDGTP-----
CONSENSUS/80%	s.t..t...splplRhssGpph.ppF..spp.lptlhthl.....s.sss.....
CONSENSUS/65%	stpptt.stsplQlRhssGpphsppFs.uppslpplhphl....t...s.ssss.....
CONSENSUS/50%	Pppps.sps+LQlRhPDGpplscCFs.us-sLcplapaV....sptpssusss.....

YJE8_YEAST	-----YLFHRNIPRVTLTRNDELKSLQEL-DLLPRSTLILEP
CONSENSUS/80%apl.pshPch.hspt-.hph.p..thhspsslll..
CONSENSUS/65%FpL.pshP+c.hsps-.ppl.ch.tlhPsuslllt.
CONSENSUS/50%FpLpsaPR+slocsD..KoLp-l.sLhPsuoLLlct

Consensus terms for the PUG domain

AAF74723	EASKLLTYADNILRNPSDEKYRSIRIGNTAFSTRLLPVRGAVECLFEMGFEEG-----
CONSENSUS/80%	tslt.LLphhcNhhpp.p-.....s..hphlh.h.tsh..h...tF.ph.....
CONSENSUS/65%	pslpsLL+h1+Nhhcc.pE.....stthpctltpl.sshphhthtFsc1.h....
CONSENSUS/50%	solccLLRh1RNlh+HhcEt.....tspp1+EplGslP-uhcpaFsssFPcLhh....

AAF74723	--ETHLIFPK
CONSENSUS/80%	...phh.h.p
CONSENSUS/65%	...phathhp
CONSENSUS/50%	...csYplss

FIGURE 2 A

UBX domain present in SEQ ID NO 2

339 KAARKKYTKSIIRVQFPDGALLQGVFLPSEPTSALYEFVSAALKEPSLEFELLHPVLVKKRVIPHF
PAAGERAVTVEEEDLVPAALLKFK 428

PUG domain present in SEQ ID NO 2:

173 GSVEVVIKLLKNIVKEPENAKFRKIRMGPNPKIKGAIGDVVGGVELLEFVGFELKEEGGEIWA VMDV
PS 240

UBX domain present in Q9ZU93

343 KAARKRYKRSMIRVQFPDGVVLQGVFAPWEPTFALYEFVSSALKEPSLQFELLDPVLVKRRVIPHT
PAPGQKPITLEDEELVPSALIRFRP 435

PUG domain present in Q9ZU93

181 SSIDVLLRLFKNIVKEPENAKFRKVRMSNAKIKEAIGDVAGGVELLELVGFELKEENDEIWA VMDV
PS 248

FIGURE 2 B

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Q9ZU93	1	MDDVKDKLKGFMKKVNLSSSSGKFKGQGRVLGSSSSSSAPPVNPIQNRFN	50
SEQ_ID_NO_2	1	MGDMKDKVKGFMKKVT-SSSSGKFKGQGRVLGGSSSSG--PSNHV-MNFS	46
Q9ZU93	51	S-----SQAPNPTPRPKPNPNPLPEKPLSSSDQKISGSTR---NPDHD	90
SEQ_ID_NO_2	47	SHPLNTRQDQPPSYT-----KTSPQKP-SNSDQRIENICEIQFNKSES	88
Q9ZU93	91	PVRAPQDGFDPYGAFITSSNRSQNGYSL-SMFECPICKNPFTSEEEVSVH	139
SEQ_ID_NO_2	89	-----KDGFDPPFGLVTSGRNPKGYSLTNVFECPCGSGFVSEEEVSTH	133
Q9ZU93	140	VESCLG---DTN-GDESSFEKDNNDNDKSEMEKLVVYLSGKPESSIDV	185
SEQ_ID_NO_2	134	IDSCLSSEVSSNLGVESKVEV-----KSELETCVSAYVSGKPEGSVEV	177
Q9ZU93	186	<u>LLRLFKNIVKEPENAKFRKVRMSNAKIKEAIGDVAGGVLELVLGFELKE</u>	235
SEQ_ID_NO_2	178	<u>VIKLLKNIVKEPENAKFRKIRMGNPKIKGAIGDVVGGVLELVLGFELKE</u>	227
Q9ZU93	236	<u>ENDEIWAVMDVPSEEQSILINKVVGYLEKRKTESSGSSAQV--MEPVAPK</u>	283
SEQ_ID_NO_2	228	<u>EGGEIWAVMDVPSEEQLVMLKNVVSLLPEPKVEELASLSQVKASEPVEPK</u>	277
Q9ZU93	284	KIDREIRVFFSVSENVASRIEVPDSFYSLSADEIKREADLRRKKIAESQL	333
SEQ_ID_NO_2	278	KIDRQIRVFFSVSPESVAAKIELPDSFFNLSREELRREAEMRKKKLEDSKL	327
Q9ZU93	334	LIPRSYKEKQAKAARKRYKRSMIRVQFPDGVVLQGVFAPWEPTFALYEFV	383
SEQ_ID_NO_2	328	LIPKSYREKQAKAARKRYTKSIIRVQFPDGALLQGVFLPSEPTSALYEFV	377
Q9ZU93	384	<u>SSALKEPSLQFELLDPVLVKRRVIPHTPAPGQKPTITLEDEELVPSALIRF</u>	433
SEQ_ID_NO_2	378	<u>SAALKEPSLEFELLHPVLVKKRVIPHPPAAGERAVTVEEEDLVPAALLKF</u>	427
Q9ZU93	434	RPIETDSLVTGLRNELLEISEPLS	458
SEQ_ID_NO_2	428	KPIETDSVVTGLCNELLEISEPLETGSVASS	459

FIGURE 2 C

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SEQ_ID_NO2	1	MGDMKDKVKGFMMKVTSSSSG---KFKGQGRVLGGSSSSGSPSNHVNNFSS	47
SEQ_ID_NO4_C	1	mmkdkmkefmkkvtsssgsgtpssfkgtshvlg---sgpsps----ss	40
SEQ_ID_NO2	48	HPL----NTRQDQQPSYTKTSPQKPSNSDQRIENICEIQFNKSESKDGF	93
SEQ_ID_NO4_C	41	hpaarssnpsnlrpapkrtsptptlttdlts-----	74
SEQ_ID_NO2	94	PFGEIVTSGKRNPKGYS---LTNVFECPCVCGSGFVSEEEVSTHIDSCLS	140
SEQ_ID_NO4_C	75	-ftplvcyssrrpdangtaCavatvacpscgdafpselavsehldgclas	123
SEQ_ID_NO2	141	EVSSNLGVESKVEVKSELETCVSAYVSG--KPSEGVSVEVIKLLKNIVKE	188
SEQ_ID_NO4_C	124	ag---garar-----aaaylaadppppaasvevvrllgnllre	159
SEQ_ID_NO2	189	PENAKFRKIRMGNPKIKGAIGDVVGVELLEFVGFEELKEEGEIVAVMD-	237
SEQ_ID_NO4_C	160	pgndkfrvrllgnpriekaladrdggvelleavqftvgdeggepfavmde	209
SEQ_ID_NO2	238	VPSEEQLVMLKNVVSLLLE-----PKKVEELASLSQVKASEPVE-PKKI	279
SEQ_ID_NO4_C	210	vpsdprlmgirravlllegahpsappvkaeaeakescsnsvdvgqegakti	259
SEQ_ID_NO2	280	DRQIRVFFSVPESSAAKIELPDSFFNLSREELRREAEMRKKKLEDSKLLI	329
SEQ_ID_NO4_C	260	drqirvfsvpgssmaqndvpdsfyklsgeeirneakmrrerleqsrlli	309
SEQ_ID_NO2	330	PKSYREKQAKAARKKYTKSIIRVQFPDGALLQGVFLPSEPTSALEYFVSA	379
SEQ_ID_NO4_C	310	pksykekqalaarqkykqavirvqfpdrmlqgqiflpgatsslyefvts	359
SEQ_ID_NO2	380	ALKEPSLEFELLHPVLVKKRVIPHFPAAGERAVTVEEEDLVPAALLKFKP	429
SEQ_ID_NO4_C	360	alkqsglefelispaipkprvvphfpnpgerartlqeeelvpsallkfip	409
SEQ_ID_NO2	430	IETDSVVFTGLCNELLEISEPLETGSVASS	459
SEQ_ID_NO4_C	410	ketdsmvftgllldellmaseplpaasq	436

FIGURE 2 D

SEQ_ID_NO_4	1	mmkdkmkdfmkkkvt--ssgsgtpssfkgtshvlsgspssshaarssn	48
SEQ_ID_NO_7	1	MMKEKMKDLMRKVTSSSSSSSSSSSFKGTAHVLGSGDPSS----RPSN	45
SEQ_ID_NO_4	49	pspnlrpapkrtspptptlttdltsftplvcyssrr--pdangtaCava	96
SEQ_ID_NO_7	46	PTPSRPAAPRREAAASARPSSSGFAPYSPLISTSSRRDTPPAGAGAGEDD	95
SEQ_ID_NO_4	97	tvacpscgdafpselavsehldgclasaggararaaaylaadppppaasv	146
SEQ_ID_NO_7	96	AVACPSCAEPFPSELAVSDHLDGCLAAAGGARPRAAAYLAGD--PPASAV	143
SEQ_ID_NO_4	147	<u>evvkrllgllrepngndkfrvrlgnprikealadrdggvellingftv</u>	196
SEQ_ID_NO_7	144	<u>EVVKRLLGNNLSDPRNDKYRKVRLGNPRIKEALADREGGVDLLEAVGFRV</u>	193
SEQ_ID_NO_4	197	<u>gdeggepfavmdevpsdprlmgirravlllegahpsappvkaeaeakesc</u>	246
SEQ_ID_NO_7	194	<u>ADEGGELFALMDEVPGDARLGGIRQAVLLLERARPSTPP-QTQADAKETC</u>	242
SEQ_ID_NO_4	247	sn-vsdvgegaktidrqirvfsvpgssmaqndvpdsfyklsgeeirnea	295
SEQ_ID_NO_7	243	PNGVSEEQGIKKPVDRQIRVFFSVAASSVAENDLPDSFYSLSNEEIRNEA	292
SEQ_ID_NO_4	296	kmrrerlegsrlipksykeqgalaarqkykqavirvqfpdrmilqgifl	345
SEQ_ID_NO_7	293	KMRERLEQSRLIPKSYKEQALAAARQKYQALIRIQFPDGVILQGVFL	342
SEQ_ID_NO_4	346	pgeatsslyefvtsalkqsglefelispaipkprvvphfnpngerartlq	395
SEQ_ID_NO_7	343	PAEPISSLYEFVASSLKQPSLEFDLICPAGPTRVIPPFFKPGEQARTLR	392
SEQ_ID_NO_4	396	eeelvpsallkfipketdsmvftglldellmaseplpaasq	436
SEQ_ID_NO_7	393	DEDLVPSARLTFKPKETDSVVFTGLLDELLETSEPFTSASS	433

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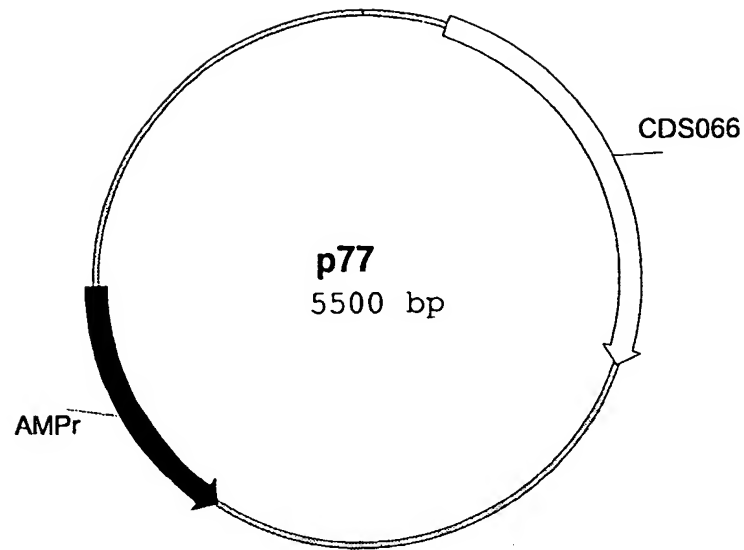


FIGURE 3

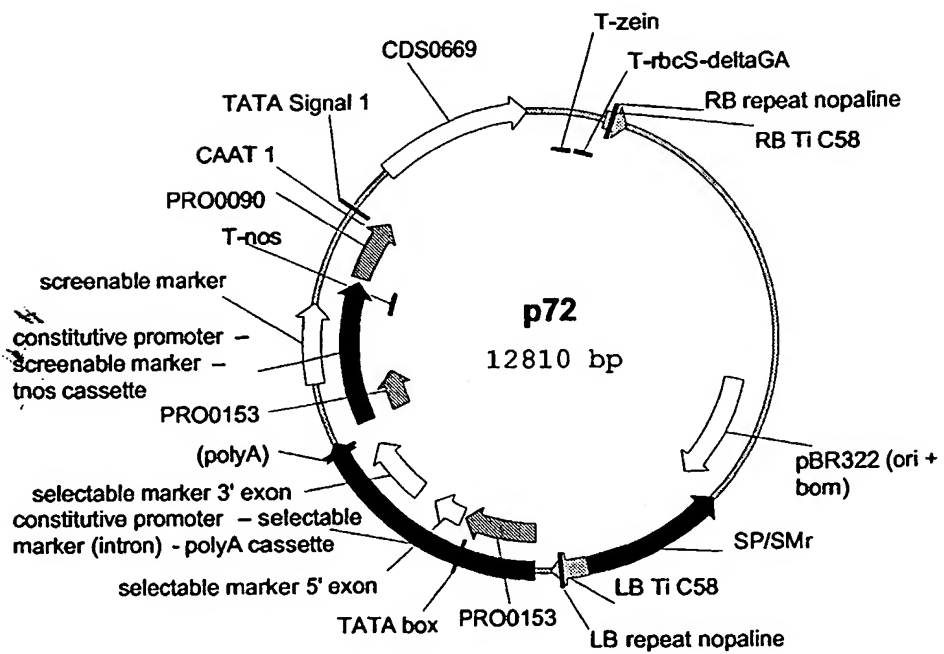


FIGURE 4

SEQ ID NO 1: GRUBX coding sequence

SEQ ID NO 2: GRUBX, deduced protein sequence

SEQ ID NO 3: GRUBX orthologue from sugarcane

FIGURE 5

SEO ID NO 4: sugarcane GRUBX orthologue, deduced protein sequence

SEQ ID NO 5: expression cassette comprising *GRU8X* (1011-2390) operably linked to the prolamine promoter (1-654) and the T-Zein + T-Rubisco deltaG terminator (2615-2808 and 2852-3048):

[illegible]

FIGURE 5 (continued)

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cagtgtgagcaatgacctgaatgaacaattgaaatgaaaagaaaaaaagtactccatctgttccaaatta
aaattcattttaaccttttaataaggtttatacaataattgatatatgttttctgtatatgtctaatttgt
tatcatccgggcgggtcttctagggataaacagggttaattatatccctctagacaacacacaacaataaga
gaaaaaacaataatattaatttgagaatgaacaaaaggaccatatcattcattaactcttctccatcca
tttccatttcacagttcgatagcgaaaaccgaataaaaaacacagtaaattacaagcacaacaatggta
caagaaaaacagttttcccaatgccataataactcgaac

SEQ ID NO 6: *Oryza sativa* GRUBX orthologue, DNA sequence

atgatgaaggaaaagatgaaggatctcatgaggaaggtcacctcctcctcctcctcctcgtcgtcct
cctccttcaaggacccgcccacgtcctcggtccggccccgacccctcctcccgcctccaacctac
ccctagtcgccccgctgccccccggcgagaggccgcccctccgagggcgccctcctcgggttcgac
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tggtgattccaaagtcatataaggagaagcaggcactggctgcccgcagagaagtataaacaagctctgat
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tatgagtttgtcgcatcttctttgaagcagccaagtttgaattcgatcttatctgtccagcgggctcta
ggacacgcgtcatacctccttttccaaaaccaggggaacaggcacgcacactgcgggatgaagacctagt
cccttctgctcggtcaccttcaagccaaagagactgattcggttggttgcactgggtctgttgagcagag
cttcttgagaccagtgaagcgttcacatctgcatcctcatga

SEQ ID NO 7: *Oryza sativa* GRUBX orthologue, deduced protein sequence

MMKEKMKDLMRKVTSSSSSSSSSSSSFKGTAHVLGSGPDPSSRPSNPTPSRPAAPRREAAASARPPSSGFA
PYSPLISTSSRRTPPAGAGAGEDDAVACPSCAEPFPSELAVSDHLDGCLAAAGGARPRAAAYLAGDPPA
SAVEVVKRLLGNLLSDPRNDKYRKVRLGNPRIKEALADREGGVDLLEAVGFRVADEGGELFALMDEVPGD
ARLGIRQAVLLLERARPSTPPQTQADAKETCPNGVSEEQGIKKPVDRQIRVFFSVAASSVAENDLPDSF
YLSNEEIRNEAKMRERLEQSRLIPKSYKEQALAAARQKYKQALIRIQFPDGVILQGVFLPAEPISSL
YEFVASSLKQPSLEFDLICPAGPRTRVIPPFPKPGEQARTLRDEDLVPSARLTFKPKETDSVVFTGLLDE
LLETSEPFTSASS

FIGURE 5 (continued)